```
<!--StartFragment-->RESULT 7
                                                           250 101001 1
PCT-US02-22833-26
                                                           PCT/USO2/22833
, Sequence 26, Application PC/TUS0222833
 GENERAL INFORMATION:
  APPLICANT: INCYTE GENOMICS, INC.
  APPLICANT: LAL, Preeti G.
APPLICANT: HONNCHELL, Cynthia D.
APPLICANT: FORSYTHE, Ian J.
  APPLICANT: WALIA, Narinder K.
  APPLICANT: TANG, Y. Tom
  APPLICANT: BOROWSKY, Mark L.
  APPLICANT: BARROSO, Ines
  APPLICANT: YUE, Henry
  APPLICANT: WARREN, Bridget A.
 APPLICANT: WARKEN, BITUGET A.

APPLICANT: THANGAVELU, Kavitha

APPLICANT: GIETZEN, Kimberly J.

APPLICANT: AZIMZAI, Yalda

APPLICANT: LEE, Ernestine A.
  APPLICANT: BAUGHN, Mariah R.
  APPLICANT: GORVAD, Ann E.
  APPLICANT: DUGGAN, Brendan M.
  APPLICANT: TRAN, Bao
  APPLICANT: LI, Joana X.
  APPLICANT: RICHARDSON, Thomas W.
  APPLICANT: ELLIOTT, Vicki S.
  APPLICANT: ZEBARJADIAN, Yeganeh
APPLICANT: TRAN, Uyen K.
APPLICANT: YAO, Monique G.
APPLICANT: PETERSON, David P.
  APPLICANT: LUO, Wen
  APPLICANT: LEHR-MASON, Patricia M.
  TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS
  FILE REFERENCE: PF-1082 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/22833
  CURRENT FILING DATE:
                           2002-07-16
  PRIOR APPLICATION NUMBER: US 60/306,020
  PRIOR FILING DATE: 2001-07-17
   PRIOR APPLICATION NUMBER: US 60/308,179
   PRIOR FILING DATE: 2001-07-27
  PRIOR APPLICATION NUMBER: US 60/309,702
 PRIOR FILING DATE: 2001-08-02
  PRIOR APPLICATION NUMBER: US 60/311,476
 PRIOR FILING DATE: 2001-08-10
  PRIOR APPLICATION NUMBER: US 60/311,718
  PRIOR FILING DATE: 2001-08-10
  PRIOR APPLICATION NUMBER: US 60/311,551
  PRIOR FILING DATE: 2001-08-10
  PRIOR APPLICATION NUMBER: US 60/314,798
  PRIOR FILING DATE: 2001-08-24
  PRIOR APPLICATION NUMBER: US 60/316,639
   PRIOR FILING DATE: 2001-08-31
  PRIOR APPLICATION NUMBER: US 60/317,996
  PRIOR FILING DATE: 2001-09-07
  NUMBER OF SEQ ID NOS: 46
 SOFTWARE: PERL Program
 SEQ ID NO 26
   LENGTH: 3320
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: misc_feature
```

OTHER INFORMATION: Incyte ID No: 566361CB1 PCT-US02-22833-26 Query Match 78.7%; Score 1954.6; DB 1; Length 3320; Best Local Similarity 87.7%; Pred. No. 0; Matches 2186; Conservative Mismatches 0; 289; Indels 18: Gaps 4; 1 ATGGCCTCAGCTGACAAGAATGGCAGCAACCTCCCATCTGTGTCTGGTAGCCGCCTGCAG 60 Qу Db 282 ATGGCCTCTGCTGACAAGAATGGCGGGAGCGTGTCCTCTGTGTCCAGCAGCCGCCTGCAG 341 61 AGCCGGAAGCCACCCAACCTCTCCATCACCATCCCGCCACC-----AGAGAGCCAGGCC 114 Qу 342 AGCCGGAAGCCACCCAACCTCTCCATCACCATCCCGCCACCCGAGAAAGAGACCCAGGCC 401 Db 115 CCCGGCGAGCAGGATAGCATGCTTCCTGAGAGGCGCAAGAACCCAGCCTACCTGAAGAGT 174 Qу 402 CCTGGCGAGCAGGACAGCATGCTGCCTGAGAGG-Db -AAGAACCCAGCCTACTTGAAGAGC 458 175 GTCAGCCTACAGGAGCCCCGGGGACGATGGCAGGAGGGGCGCAGAGAAGCGCCCCGGCTTC 234 Qу 111111111111 459 GTCAGCCTCCAGGAGCCACGCAGCCGATGGCAGGAGAGTTCAGAGAAGCGCCCTGGCTTC 518 Db 235 CGCCGCCAGGCCTCCCTGTCCCAGAGCATCCGCAAGAGCACAGCCCAGTGGTTTGGGGTC 294 Qу CGCCGCCAGGCCTCACTGTCCCAGAGCATCCGCAAGGGCGCAGCCCAGTGGTTTGGAGTC 578 Db ·295 AGCGGCGACTGGGAGGGCAAGCGACAAAACTGGCATCGTCGCAGCCTGCACCACTGCAGC 354 Qу 579 AGCGGCGACTGGGAGGGGCAGCAGCAGCGCGCAGCCTGCACCACTGCAGC 638 Db Qy Db 415 GTGCCATCCTTCCAGGGCACTGAGTCTCCAAAACCGTGCAAGATGCCCAAGATTGTGGAT 474 Qу Db 699 GCACCGTCCTTCCAGGGCACTGAGTCCCCAAAGCCCTGCAAGATGCCCAAGATTGTGGAT 758 475 CCACTGGCTCGGGGTAGGGCCTTCCGCCATCCAGATGAGGTGGACCGGCCTCACGCTGCC 534 Qу Db CCGCTGGCCCGGGGCCGGCCTTCCGCCACCCGGAGGAGATGGACAGGCCCCACGCCCTG 818 535 CACCCACCTCTGACTCCAGGGGTCCTGTCTCTCACATCCTTCACCAGTGTCCGCTCTGGC 594 Qу Db CACCCACCGCTGACCCCCGGAGTCCTGTCCCTCACCTCCTTCACCAGTGTCCGTTCTGGC TACTCCCATCTGCCCCGCCGCAAGAGGATATCTGTTGCCCATATGAGCTTTCAGGCAGCC 654 Qу TACTCCCACCTGCCACGCCGCAAGAGAATGTCTGTGGCCCACATGAGCTTGCAAGCTGCC 938 Db 655 GCCGCCCTCCAAGGGGCGTTCCGTGCTAGATGCGACTGGGCAGCGGTGCCGGCATGTC 714 Qу 939 GCTGCCCTCCTCAAGGGGCGCTCGGTGCTGGATGCCACCGGACAGCGGTGCCGGGTGGTC 998 Db Qу 715 AAACGCAGCTTCGCTTACCCCAGCTTCCTGGAGGAGGATGCTGTCGATGGAGCTGACACC 774 999 AAGCGCAGCTTTGCCTTCCCGAGCTTCCTGGAGGAGGATGTGGTCGATGGGGCAGACACG 1058 Db 775 TTCGACTCCTCTTTTTAGTAAGGAAGAAATGAGCTCCATGCCTGACGATGTCTTTGAG 834 Qу 

Db	1059	$\tt TTTGACTCCTCTTTTTTAGTAAGGAAGAAATGAGCTCCATGCCTGATGATGTCTTTGAG$	1118
Qy	835	TCCCCCCACTCTCTGCCAGCTACTTCCGAGGTGTCCCACACTCTGCCTCCCCGGTCTCC	894
Db	1119		1178
Qу	895	CCGGATGGAGTGCACATCCCGCTAAAAGAATACAGCGGTGGCCGAGCCCTGGGTCCCGGG	954
Db	1179		1232
Qy	955	ACCCAGCGTGGCAAACGCATTGCCTCCAAAGTAAAGCACTTTGCATTTGACCGGAAGAAG	1014
Db	1233		1292
Qy	1015	AGGCACTACGGCCTGGGTGTCGTGGGTAACTGGCTCAACCGAAGCTATCGACGCAGCATC	1074
Db	1293		1352
Qy	1075		1134
Dḃ	1353		1412
Qу	1135	TGGCTGACGTTCACATCATCATCACCTTGCTGGTGATCTGCACCTATGGCATCGCA	1194
Db	1413		1472
Qy	1195	${\tt CCTGTGGGCTTTGCCCAGCAGGTTACCACCCAGCTGGTGCTGAAGAACAGAGGCGTGTAT}$	1254
Db	1473		1532
Qy	1255		1314
Db	1533		1592
Qy	1315	ATTCACCTGGGAGCAAAGTTCTCGCCCTGCATCCGGAAGGACCAGCAAATTGAGCAGCTG	1374
Db	1593		1652
Qy	1375	GTACGGAGGGAGCGCACATTGAGCGCACCTCTGGCTGCTGTGTCCAGAATGACCGCTCG	1434
Db	1653		1712
Qy	1435	GGCTGCATCCAGACCCTGAAGAAGGACTGCTCGGAGACTTTAGCCACGTTCGTAAAGTGG	1494
Db	1713	GGATGCATCCAGACCCAGCGGAAGGACTGCTCGGAGACTTTGGCCACTTTTGTCAAGTGG	1772
Qy	1495	CAGAATGATACTGGGCCCTCAGACAAGTCTGACCTGAGCCAGAAGCAGCCATCGGCG	1551
Db	1773		1832
Qy	1552	GTTGTGTGCCACCAAGACCCCAGGACCTGTGAAGAGCCTGCCT	1611
Db	1833	GCTGTCTGCCACCAGGACCCCAGGACCTGCGAGGAGCCAGCC	1892
Qy	1612	TGGCCTGATGACATTACCAAGTGGCCGATCTGCACAGAGCAGGCTCAGAGCAACCACACG	1671
Db	1893	TGGCCCGATGACATCACTAAGTGGCCGATCTGCACAGAGCAGGCCAGGAGCAACCACACA	1952
Qу	1672	GGCTTGTTGCACATAGACTGTAAGATCAAAGGCCGCCCCTGCTGCATCGGCACCAAGGGC	1731
Db	1953		2012

•			
Qy	1732	AGCTGCGAGATCACCACTCGGGAGTACTGTGAGTTCATGCATG	1791
Db	2013	AGCTGTGAGATCACCACCCGGGAATACTGTGAGTTCATGCACGGCTATTTCCATGAGGAA	2072
Qу	1792	GCGACGCTGTGTTCCCAGGTGCACTGTTTAGACAAGGTGTGTGGGCTCCTGCCTTTCCTC	1851
Db	2073	GCAACACTCTGCTCCCAGGTGCACTGCTTGGACAAGGTGTGTGGGCTGCCCTTCCTC	2132
Qy	1852	AACCCTGAGGTCCCTGACCAGTTCTACCGGATCTGGCTGTCTTTATTCCTGCATGCTGGC	1911 .
Db	2133	AACCCTGAGGTCCCAGATCAGTTCTACAGGCTCTGGCTGTCTCTTCCTACATGCTGGC	2192
Qy	1912	ATAGTGCACTGCCTTGTGTCTTGTGGTCTTCCAAATGACCATCCTGAGGGACCTAGAGAAG	1971
Db	2193	GTGGTGCACTGCCTCGTGTCTTGTGGTCTTTCAAATGACCATCCTGAGGGACCTGGAGAAG	2252
Qу	1972	CTGGCCGGCTGGCACCGCATCTCCATCATCTTCATCCTTAGTGGCATTACAGGCAACCTG	2031
Db	2253	CTGGCCGGCTGGCACCGTATCGCCATCATCTTCATCCTCAGTGGCATCACAGGCAACCTC	2312
Qу	2032	GCCAGCGCCATCTTCCTCCCCTACCGGGCAGAGGTGGGCCCAGCCGGGTCGCAGTTCGGC	2091
Db	2313	GCCAGTGCCATCTTTCTCCCATACCGGGCAGAGGTGGGCCCGGCCGG	2372
Qy	2092	CTCCTCGCCTGCCTCTTCGTGGAGCTGTTCCAGAGCTGGCAGCTGTTGGAGCGGCCGTGG	2151
Db	2373	CTCCTCGCCTGCCTCTTCGTGGAGCTCTTCCAGAGCTGGCCGCTGCTGGAGAGGCCCTGG	2432
Qу	2152	AAGGCCTTCTTCAACCTGTCGGCCATTGTGCTTTTCCTCTTCATCTGTGGCCTCCTGCCC	2211
Db	2433	AAGGCCTTCCTCAACCTCTCGGCCATCGTGCTCTTCCTGTTCATCTGTGGCCTCCTGCCC	2492
Qу	2212	TGGATAGACAACATCGCCCACATCTTCGGGTTCCTCAGCGGCATGCTTCTGGCCTTCGCC	2271
Db	2493	TGGATCGACAACATCGCCCACATCTTCGGCTTCCTCAGTGGCCTGCTGCTGCCTTCGCC	2552
Qy	2272	TTCCTGCCTTACATTACCTTCGGCACCAGCGACAAGTACCGCAAGCGAGCCCTCATCCTC	2331
Db		TTCCTGCCCTACATCACCTTCGGCACCAGCGACAAGTACCGCAAGCGGGCACTCATCCTG	
Qу		GTGTCGCTGCTGGTCTTTGCTGGGCTCTTTGCTTCCCTGGTGCTGTGCTGTACATCTAC	
Db	2613	GTGTCACTGCCGCCCTCTTCGCCGCCCTCGTGCTGTGCT	2672
Qу		CCCATCAACTGGCCCTGGATCGAGTACCTCACCTGCTTTCCCTTCACCAGCCGCTTCTGT	
Db	2673	CCCATTAACTGGCCCTGGATCGAGCACCTCACCTGCTTCCCCTTCACCAGCCGCTTCTGC	2732
Qу	2452	GAGAAGTACGAGCTAGACCAGGTGCTACACTAA 2484	
Db	2733	GAGAAGTATGAGCTGGACCAGGTGCTGCACTGA 2765	

<!--EndFragment-->

## SEQ ID 1012

```
<!--StartFragment-->RESULT 3
                                                 WO 2003027228-A2
TD
     ADC42843 standard; protein; 827 AA.
XX
AC
     ADC42843;
XX
DT
     18-DEC-2003
                  (first entry)
XX
DE ·
     REMAP protein #3.
XX
KW
     Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;
KW
     Antiallergic; Antidiabetic; REMAP; pathogenesis.
XX
os
     Homo sapiens.
XX
PN
     WO2003027228-A2.
XX
PD
     03-APR-2003.
XX
PF
     16-JUL-2002; 2002WO-US022833.
XX.
PR
     17-JUL-2001; 2001US-0306020P.
PR
     27-JUL-2001; 2001US-0308179P.
     02-AUG-2001; 2001US-0309702P.
PR
     10-AUG-2001; 2001US-0311476P.
PR
     10-AUG-2001; 2001US-0311551P.
PR
     10-AUG-2001; 2001US-0311718P.
PR
     24-AUG-2001; 2001US-0314798P.
PR
PR
     31-AUG-2001; 2001US-0316639P.
PR
     07-SEP-2001; 2001US-0317996P.
XX
PA
     (INCY-) INCYTE GENOMICS INC.
XX
     Lal PG, Honchell CD, Forsythe IJ, Walia NK, Tang TY, Borowsky ML;
ΡI
ΡI
     Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;
     Lee EA; Baughn MR, Gorvad AE, Duggan BM, Tran B,
PΙ
     Richardson TW, Elliott VS, Zebarjadian Y, Tran UK, Yao MG;
PI
ΡI
     Peterson DP, Luo W, Lehr-Mason PM;
XX
DR
     WPI; 2003-421156/39.
XX
PT
     New human receptors and membrane-associated proteins (REMAP), useful for
PT
     diagnosing, treating or preventing disorders associated with aberrant
PT
     REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or
PT
     stroke.
XX
PS
     Claim 1; SEQ ID NO 3; 115pp; English.
XX
     The present invention relates to an isolated polypeptide. The.
CC
CC
     polypeptides and polynucleotides are useful in diagnosing, treating and
CC
     preventing disorders associated with aberrant expression of REMAP, such
CC.
     as cell proliferative, autoimmune/inflammatory, renal, neurological,
     cardiovascular, metabolic, developmental, endocrine, muscle,
CC
CC
     gastrointestinal, lipid metabolism or transport disorders, and viral
CC
     infections. These are also useful in assessing the effects of exogenous
CC
     compounds on the expression of nucleic acids and amino acid sequences of
CC
     REMAP, in facilitating drug discovery process, and in investigating the
CC
     pathogenesis of diseases or medical conditions. Expression and
CC
     purification were achieved using bacterial or virus-based expression
CC
     systems. The present sequence represents an REMAP protein of the
CC
    .invention.
```

```
XX
SQ
   Sequence 827 AA;
 Query Match
                   92.1%;
                        Score 4088; DB 7; Length 827;
 Best Local Similarity
                   91.6%;
                        Pred. No. 0;
       760:
            Conservative
                       31;
                           Mismatches
                                        Indels
                                    33;
                                               6;
                                                  Gaps
                                                        4;
         1 MASADKNGSNLPSVSGSRLQSRKPPNLSITIPPP--ESQAPGEQDSMLPERRKNPAYLKS 58
Qу
          Db
        1 MASADKNGGSVSSVSSSRLQSRKPPNLSITIPPPEKETQAPGEQDSMLPE-RKNPAYLKS 59
Qу
        59 VSLQEPRGRWQEGAEKRPGFRRQASLSQSIRKSTAQWFGVSGDWEGKRQNWHRRSLHHCS 118
          Db
         VSLQEPRSRWQESSEKRPGFRRQASLSQSIRKGAAQWFGVSGDWEGQRQQWQRRSLHHCS 119
       119 VHYGRLKASCQRELELPSQEVPSFQGTESPKPCKMPKIVDPLARGRAFRHPDEVDRPHAA 178
Qу
          120 MRYGRLKASCQRDLELPSQEAPSFQGTESPKPCKMPKIVDPLARGRAFRHPEEMDRPHAL 179
Db
         HPPLTPGVLSLTSFTSVRSGYSHLPRRKRISVAHMSFQAAAALLKGRSVLDATGQRCRHV 238
Qу
          HPPLTPGVLSLTSFTSVRSGYSHLPRRKRMSVAHMSLQAAAALLKGRSVLDATGQRCRVV 239
Db
         KRSFAYPSFLEEDAVDGADTFDSSFFSKEEMSSMPDDVFESPPLSASYFRGVPHSASPVS 298
Qу
          Db
          KRSFAFPSFLEEDVVDGADTFDSSFFSKEEMSSMPDDVFESPPLSASYFRGIPHSASPVS 299
       299 PDGVHIPLKEYSGGRALGPGTQRGKRIASKVKHFAFDRKKRHYGLGVVGNWLNRSYRRSI 358
Qу
          300 PDGVQIPLKEY--GRAPVPGPRRGKRIASKVKHFAFDRKKRHYGLGVVGNWLNRSYRRSI 357
Db
Qу
       359 SSTVQRQLESFDSHRPYFTYWLTFVHIIITLLVICTYGIAPVGFAQHVTTQLVLKNRGVY 418
          358 SSTVQRQLESFDSHRPYFTYWLTFVHVIITLLVICTYGIAPVGFAQHVTTQLVLRNKGVY 417
Db
       419 ESVKYIQQENFWIGPSSIDLIHLGAKFSPCIRKDQQIEQLVRRERDIERTSGCCVQNDRS 478
Qу
          Db
       418 ESVKYIQQENFWVGPSSIDLIHLGAKFSPCIRKDGQIEQLVLRERDLERDSGCCVQNDHS 477
         GCIQTLKKDCSETLATFVKWQNDTG-PSDKSDLSQKQPSAVVCHQDPRTCEEPASSGAHI 537
Qу
          GCIQTQRKDCSETLATFVKWQDDTGPPMDKSDLGQKRTSGAVCHQDPRTCEEPASSGAHI 537
Db
         WPDDITKWPICTEQAQSNHTGLLHIDCKIKGRPCCIGTKGSCEITTREYCEFMHGYFHED 597
Qу
          Db
          WPDDITKWPICTEQARSNHTGFLHMDCEIKGRPCCIGTKGSCEITTREYCEFMHGYFHEE 597
       598 ATLCSQVHCLDKVCGLLPFLNPEVPDQFYRIWLSLFLHAGIVHCLVSVVFQMTILRDLEK 657
Qу
          ATLCSQVHCLDKVCGLLPFLNPEVPDQFYRLWLSLFLHAGVVHCLVSVVFQMTILRDLEK 657
Db
Qy
       658 LAGWHRISIIFILSGITGNLASAIFLPYRAEVGPAGSQFGLLACLFVELFQSWQLLERPW 717
          658 LAGWHRIAIIFILSGITGNLASAIFLPYRAEVGPAGSQFGLLACLFVELFQSWPLLERPW 717
Db
Qу
       718 KAFFNLSAIVLFLFICGLLPWIDNIAHIFGFLSGMLLAFAFLPYITFGTSDKYRKRALIL 777
          Db
       718 KAFLNLSAIVLFLFICGLLPWIDNIAHIFGFLSGLLLAFAFLPYITFGTSDKYRKRALIL 777
       778 VSLLVFAGLFASLVLWLYIYPINWPWIEYLTCFPFTSRFCEKYELDQVLH 827
Qу
```

778 VSLLAFAGLFAALVLWLYIYPINWPWIEHLTCFPFTSRFCEKYELDQVLH 827

<!--EndFragment-->

Db